

REMARKS

Introductory Comments

Reconsideration of the above-identified application in view of the foregoing arguments is respectfully requested.

Claims 52-81 are pending. Claims 62-69 and 71-76 remain withdrawn from consideration. Claims 52-61, 70 and 77-81 are under consideration.

Rejection of Claims 52-61, 70 and 77-81 Under 35 U.S.C. § 101

And § 112, First Paragraph

Claims 52-61, 70 and 77-81 are rejected under 35 U.S.C. § 101 and § 112, first paragraph, for the reason contained in the previous Office Action. The Examiner contends that the Declaration of Dr. Granados is germane to the rejection at issue and that it fails to provide any evidence that the BS322 polypeptides according to SEQ ID NOS: 25-28 are equivalent to the NY-BR-1 breast cancer antigen polypeptide. Applicants respectfully traverse this rejection.

As submitted by Applicants in their previous responses, the Dirk Jager *et al.* article "Identification of Tissue-specific Putative Transcription Factor..." support Applicants' contention that SEQ ID NOS: 24-28 as claimed are useful as required by 35 U.S.C. § 101 and § 112, first paragraph. The Jager *et al.* article shows that the gene NY-BR-1 is one of the genes responsible for breast cancer. The gene has 37 exons. See the abstract. Applicants have shown in previous responses in Exhibit A, the 100% alignment match and homology between NY-BR-1 and a nucleotide sequence designated BS322 (SEQ ID NO: 9). Nucleotide sequence BS322 or SEQ ID NO: 9 as described in the instant specification, encodes the polypeptide sequences designated SEQ ID NOS: 24-28. These polypeptides are useful in the detection of breast disease which Examiner has refuted.

The Examiner contends in the previous Office Actions that the alignment match between BS322 and NY-BR-1 does not prove that BS322 is the same molecule as NY-BR-1 since 1143 nucleotides are unaccounted for. The Examiner uses this single basis to support her reason why SEQ ID NOS: 24-28 are not useful in the detection of breast disease. Although Applicants appreciate the Examiner's detailed analysis, Applicants respectfully traverse the rejection and contend this line of reasoning is flawed for the reason set forth below.

Applicants agree with the Examiner's observation that the alignment consensus between BS322 and NY-BR-1 does not prove BS322 is the exact same molecule of NY-BR-1. However, the 100% consensus between these two molecules over one thousand nucleotides indicates that BS322 could be a splice variant of NY-BR-1. Applicants have attached herein a portion of a BLAST result for AF269087 (NY-BR-1) versus the human genome. As the Examiner can see, the junctions of the exons for the gaps match those that are in the BS322 molecule. Specifically, three exons that account for gaps are at the positions of 3013-3200, 3197-4116 and 2796-3014. This information clearly provides evidence that BS322 is a splice variant of NY-BR-1.

As indicated in the Jager *et al.* article, NY-BR-1 comprises 37 exons. Exons, also known as expressed sequences, are defined as a portions of a gene

that appear in both the primary and mature mRNA transcripts (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999). Thus, one of ordinary skill in the art would recognize that although BS322 is not the exact molecule of NY-BR-1, the fact that there is a 100% consensus homology between the two molecules for over 1000 nucleotides of the exons indicates that one is a splice of another and would have significant commonalities. It is well known in the art that introns may be excluded from splices which maintain the functionality of a gene. An intron, also called an intervening sequence, is defined in the art as a part of a primary transcript, or DNA encoding it, that is removed by splicing during RNA processing and is not included in the mature, functional mRNA, rRNA or tRNA (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999).

As disclosed in the specification, SEQ ID NOS: 24-28 are derived from the BS322 molecule. As shown in Jager *et al.*, *supra*, and in Applicants' disclosure, mRNA expressions of the gene, i.e., sequence segments from the genes which encode proteins that have a specific epitope, are useful as markers for breast diseases. Thus, for these reasons, Applicants respectfully request the Examiner to withdraw the rejection of claims 52-61, 70 and 77- 35 under 35 U.S.C. § 101 and § 112, first paragraph, and allow the claims.

CONCLUSION

Applicants respectfully submit that the claims comply with the requirements of 35 U.S.C. Sections 101, 112, 102 and 103. Accordingly, a Notice of Allowance is believed in order and is respectfully requested.

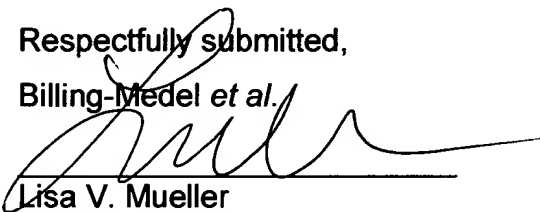
Should the Examiner have any questions concerning the above, she is respectfully requested to contact the undersigned at the telephone number listed below. If the Examiner notes any further matters which the Examiner believes may be expedited by a telephone interview, the Examiner is requested to contact the undersigned.

If any additional fees are incurred as a result of the filing of this paper, authorization is given to charge deposit account no. 23-0785.

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Respectfully submitted,
Billing-Medel et al.



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Attorney for Applicants

BS322 Contig summary1.TXT

Summary View of Contig "Contig[0013]"

>AF269087	#1	CTAGTCTATA CCAGCAACGA CTCCTACATC
	#1 CTAGTCTATA CCAGCAACGA CTCCTACATC
>AF269087	#31	GTCCACTCTG GGGATCTTAG AAAGATCCAT
	#31 GTCCACTCTG GGGATCTTAG AAAGATCCAT
>AF269087	#61	AAAGCTGCCT CCCGGGGACA AGTCCGGAAG
	#61 AAAGCTGCCT CCCGGGGACA AGTCCGGAAG
>AF269087	#91	CTGGAGAAGA TGACAAAGAG GAAGAAGACC
	#91 CTGGAGAAGA TGACAAAGAG GAAGAAGACC
>AF269087	#121	ATCAACCTTA ATATACAAGA CGCCCAGAAG
	#121 ATCAACCTTA ATATACAAGA CGCCCAGAAG
>AF269087	#151	AGGACTGCTC TACTCTGGGC CTGTGTCAAT
	#151 AGGACTGCTC TACTCTGGGC CTGTGTCAAT
>AF269087	#181	GGCCATGAGG AAGTAGTAAC ATTTCTGGTA
	#181 GGCCATGAGG AAGTAGTAAC ATTTCTGGTA
>AF269087	#211	GACAGAAAGT GCCAGCTTGA CGTCCTTGAT
	#211 GACAGAAAGT GCCAGCTTGA CGTCCTTGAT
>AF269087	#241	GGCGAACACA GGACACCTCT GATGAAGGCT
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BS322 Contig summary1.TXT

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BS322 Contig summary1.TXT

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	#901	ACACCTGATG AGGCTGCATC CTTGGTGGAG
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BS322 Contig summary1.TXT

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BS322 Contig summary1.TXT

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                .....

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BS322 Contig summary1.TXT

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		*		
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BS322 Contig summary1.TXT

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BS322 Contig summary1.TXT

>AF269087	#2491	GTTTCTATTC CAACTAAAGC CTTAGAATTG
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BS322 Contig summary1.TXT

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	#2971 GAGAACCAAA AAGTTAAATG GGAACAAGAG
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	#3001 CTCTGCAGTG TGAGATTGAC TTTAAACCAA
>AF269087	#3031	GAAGAAGAGA AGAGAAGAAA TGCCGATATA
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BS322 Contig summary1.TXT

>AF269087	#3151	AGAATACAAG ATATAGAATT GAAGAGTGTA
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		AGAATACAAG ATATAGAATT GAAGAGTGTA
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	#3181
		GAAAGTAATT TGAATCAGGT TTCTCACACT
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	#3211
		CATGAAAATG AAAATTATCT CTTACATGAA
>BS322 1199 to 2683	#43	AATTGCATGT TGAAAAAGGA AATTGCCATG
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>BS322 1199 to 2683	#73	CTAAAACTGG AAATAGCCAC ACTGAAACAC
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		CAATACCAGG AAAAGGAAAA TAAATACTTT
>BS322 1199 to 2683	#133	GAGGACATTA AGATTTTAAA AGAAAAGAAT
>AF269087	#3331	GAGGACATTA AGATTTTAAA AGAAAAGAAT
	#3331
		GAGGACATTA AGATTTTAAA AGAAAAGAAT
>BS322 1199 to 2683	#163	GCTGAACTTC AGATGACCCT AAAACTGAAA
>AF269087	#3361	GCTGAACTTC AGATGACCCT AAAACTGAAA
	#3361
		GCTGAACTTC AGATGACCCT AAAACTGAAA
>BS322 1199 to 2683	#193	GAGGAATCAT TAACTAAAAG GGCATCTCAA
>AF269087	#3391	GAGGAATCAT TAACTAAAAG GGCATCTCAA
	#3391
		GAGGAATCAT TAACTAAAAG GGCATCTCAA
>BS322 1199 to 2683	#223	TATAGTGGGC AGCTTAAAGT TCTGATAGCT
>AF269087	#3421	TATAGTGGGC AGCTTAAAGT TCTGATAGCT
	#3421
		TATAGTGGGC AGCTTAAAGT TCTGATAGCT
>BS322 1199 to 2683	#253	GAGAACACAA TGCTCACTTC TAAATTGAAG
>AF269087	#3451	GAGAACACAA TGCTCACTTC TAAATTGAAG

BS322 Contig summary1.TXT

```

#3451          .....
          GAGAACACAA TGCTCACTTC TAAATTGAAG

>BS322 1199 to 2683 #283      GAAAAACAAG ACAAAGAAAT ACTAGAGGCA
>AF269087          #3481      GAAAAACAAG ACAAAGAAAT ACTAGAGGCA
          #3481          .....
          GAAAAACAAG ACAAAGAAAT ACTAGAGGCA

>BS322 1199 to 2683 #313      GAAATTGAAT CACACCATCC TAGACTGGCT
>AF269087          #3511      GAAATTGAAT CACACCATCC TAGACTGGCT
          #3511          .....
          GAAATTGAAT CACACCATCC TAGACTGGCT

>BS322 1199 to 2683 #343      TCTGCTGTAC AAGACCATGA TCAAATTGTG
>AF269087          #3541      TCTGCTGTAC AAGACCATGA TCAAATTGTG
          #3541          .....
          TCTGCTGTAC AAGACCATGA TCAAATTGTG

>BS322 1199 to 2683 #373      ACATCAAGAA AAAGTCAAGA ACCTGCTTTC
>AF269087          #3571      ACATCAAGAA AAAGTCAAGA ACCTGCTTTC
          #3571          .....
          ACATCAAGAA AAAGTCAAGA ACCTGCTTTC

>BS322 1199 to 2683 #403      CACATTGCAG GAGATGCTTG TTTGCAAAGA
>AF269087          #3601      CACATTGCAG GAGATGCTTG TTTGCAAAGA
          #3601          .....
          CACATTGCAG GAGATGCTTG TTTGCAAAGA

>BS322 1199 to 2683 #433      AAAATGAATG TTGATGTGAG TAGTACGATA
>AF269087          #3631      AAAATGAATG TTGATGTGAG TAGTACGATA
          #3631          .....
          AAAATGAATG TTGATGTGAG TAGTACGATA

>BS322 1199 to 2683 #463      TATAACAATG AGGTGCTCCA TCAACCACTT
>AF269087          #3661      TATAACAATG AGGTGCTCCA TCAACCACTT
          #3661          .....
          TATAACAATG AGGTGCTCCA TCAACCACTT

>BS322 1199 to 2683 #493      TCTGAAGCTC AAAGGAAATC CAAAAGCCTA
>AF269087          #3691      TCTGAAGCTC AAAGGAAATC CAAAAGCCTA
          #3691          .....
          TCTGAAGCTC AAAGGAAATC CAAAAGCCTA

>BS322 1199 to 2683 #523      AAAATTAATC TCAATTATGC AGGAGATGCT
>AF269087          #3721      AAAATTAATC TCAATTATGC AGGAGATGCT
          #3721          .....
          AAAATTAATC TCAATTATGC AGGAGATGCT

>BS322 1199 to 2683 #553      CTAAGAGAAA ATACATTGGT TTCAGAACAT
>AF269087          #3751      CTAAGAGAAA ATACATTGGT TTCAGAACAT
          #3751          .....
          CTAAGAGAAA ATACATTGGT TTCAGAACAT

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BS322 Contig summary1.TXT

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>BS322 1199 to 2683 #583      GCACAAAGAG ACCAACGTGA AACACAGTGT
>AF269087              #3781    GCACAAAGAG ACCAACGTGA AACACAGTGT
                               .....
                               GCACAAAGAG ACCAACGTGA AACACAGTGT

>BS322 1199 to 2683 #613      CAAATGAAGG AAGCTGAACA CATGTATCAA
>AF269087              #3811    CAAATGAAGG AAGCTGAACA CATGTATCAA
                               .....
                               CAAATGAAGG AAGCTGAACA CATGTATCAA

>BS322 1199 to 2683 #643      AACGAACAAG ATAATGTGAA CAAACACACT
>AF269087              #3841    AACGAACAAG ATAATGTGAA CAAACACACT
                               .....
                               AACGAACAAG ATAATGTGAA CAAACACACT

>BS322 1199 to 2683 #673      GAACAGCAGG AGTCTCTAGA TCAGAAATTA
>AF269087              #3871    GAACAGCAGG AGTCTCTAGA TCAGAAATTA
                               .....
                               GAACAGCAGG AGTCTCTAGA TCAGAAATTA

>BS322 1199 to 2683 #703      TTTCAACTAC AAAGCAAAAA TATGTGGCTT
>AF269087              #3901    TTTCAACTAC AAAGCAAAAA TATGTGGCTT
                               .....
                               TTTCAACTAC AAAGCAAAAA TATGTGGCTT

>BS322 1199 to 2683 #733      CAACAGCAAT TAGTTCATGC ACATAAGAAA
>AF269087              #3931    CAACAGCAAT TAGTTCATGC ACATAAGAAA
                               .....
                               CAACAGCAAT TAGTTCATGC ACATAAGAAA

>BS322 1199 to 2683 #763      GCTGACAACA AAAGCAAGAT AACAATTGAT
>AF269087              #3961    GCTGACAACA AAAGCAAGAT AACAATTGAT
                               .....
                               GCTGACAACA AAAGCAAGAT AACAATTGAT

>BS322 1199 to 2683 #793      ATTCATTTTC TTGAGAGGAA AATGCAACAT
>AF269087              #3991    ATTCATTTTC TTGAGAGGAA AATGCAACAT
                               .....
                               ATTCATTTTC TTGAGAGGAA AATGCAACAT

>BS322 1199 to 2683 #823      CATCTCCTAA AAGAGAAAAA TGAGGAGATA
>AF269087              #4021    CATCTCCTAA AAGAGAAAAA TGAGGAGATA
                               .....
                               CATCTCCTAA AAGAGAAAAA TGAGGAGATA

>BS322 1199 to 2683 #853      TTTAATTACA ATAACCATTT AAAAAACCGT
>AF269087              #4051    TTTAATTACA ATAACCATTT AAAAAACCGT
                               .....
                               TTTAATTACA ATAACCATTT AAAAAACCGT

>BS322 1199 to 2683 #883      ATATATCAAT ATGAAAAAGA GAAAGCAGAA
>AF269087              #4081    ATATATCAAT ATGAAAAAGA GAAAGCAGAA

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BS322 Contig summary1.TXT

```

#4081      .....
            ATATATCAAT ATGAAAAAGA GAAAGCAGAA

>BS322 1199 to 2683 #913      ACAGAAAAC T CATGAGAGAC AAGCAGTAAG
>AF269087      #4111      ACAGAAAAC T CATGAGAGAC AAGCAGTAAG
            .....
            ACAGAAAAC T CATGAGAGAC AAGCAGTAAG

>BS322 1199 to 2683 #943      AAACTTCTTT TGGAGAAACA ACAGACCAGA
>AF269087      #4141      AAACTTCTTT TGGAGAAACA ACAGACCAGA
            .....
            AAACTTCTTT TGGAGAAACA ACAGACCAGA

>BS322 1199 to 2683 #973      TCTTTACTCA CAACTCATGC TAGGAGGCCA
>AF269087      #4171      TCTTTACTCA CAACTCATGC TAGGAGGCCA
            .....
            TCTTTACTCA CAACTCATGC TAGGAGGCCA

>BS322 1199 to 2683 #1003     GTCCTAGCAT CACCTTATGT TGAAAATCTT
>AF269087      #4201      GTCCTAGCAT CACCTTATGT TGAAAATCTT
            .....
            GTCCTAGCAT CACCTTATGT TGAAAATCTT

>BS322 1199 to 2683 #1033     ACCAATAGTC TGTGTCAACA GAATACTTAT
>AF269087      #4231      ACCAATAGTC TGTGTCAACA GAATACTTAT
            .....
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>BS322 1199 to 2683 #1063     TTTAGAAGAA AAATTCATGA TTTCTTCCTG
>AF269087      #4261      TTTAGAAGAA AAATTCATGA TTTCTTCCTG
            .....
            TTTAGAAGAA AAATTCATGA TTTCTTCCTG

>BS322 1199 to 2683 #1093     AAGCCTACAG ACATAAAATA ACAGTGTGAA
>AF269087      #4291      AAGCCTACAG ACATAAAATA ACAGTGTGAA
            .....
            AAGCCTACAG ACATAAAATA ACAGTGTGAA

>BS322 1199 to 2683 #1123     GAATTACTTG TTCACGAA:T :C:TCGCTCT
>AF269087      #4321      GAATTACTTG TTCACGAATT GCATAAAGCT
            .....
            GAATTACTTG TTCACGAATT GCATMRMKCT
                               * * * ****

>BS322 1199 to 2683 #1153     GCACTCCA:G CCTAGGCGCC TAGTGAAACC
>AF269087      #4351      GCACAGGATT CCCATCTACC CTGATGATGC
            .....
            GCACWSSATK CCYAKSYRCC YWGWKRAWSC
            *** ** * **** ** ** **

>BS322 1199 to 2683 #1183     CTGTGTCA:A AAAGAAAA:A AACAAAAACA
>AF269087      #4381      AGCAGACATC ATTCAATCCA ACCAGAATCT
            .....
            MKSWGWCATM AWWSAAWMCA AMCARAAWCW
            **** * ** *** ** * *

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BS322 Contig summary1.TXT

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>BS322 1199 to 2683 #1213
>AF269087 #4411
#4411
AACT:TCCAA GAC:CTCGA: GTGGTTTTTG
CGCTCTGCAC TCCAGCCTAG GTGACAGAGT
.....
MRCTCTSCAM KMCASYCKAG GTGRYWKWK
** * * * ** *** * * *****

>BS322 1199 to 2683 #1243
>AF269087 #4441
#4441
GAGACCCTGT ATCACTTCAA ATAATGTGTT
GAGACTCCAC CTCGAAA
.....
GAGACYCYRY MTCRSWMAA ATAATGTGTT
* *** * *****

>BS322 1199 to 2683 #1273
#4471
AAACAAGCAT CTTCATCTCA TTAAATAGAA
.....
AAACAAGCAT CTTCATCTCA TTAAATAGAA

>BS322 1199 to 2683 #1303
#4501
ATGTTGAAAA ATTGCTTTTG GAATAATTGA
.....
ATGTTGAAAA ATTGCTTTTG GAATAATTGA

>BS322 1199 to 2683 #1333
#4531
CTTATGGATA TTTCATCAAA TTTACAGTTG
.....
CTTATGGATA TTTCATCAAA TTTACAGTTG

>BS322 1199 to 2683 #1363
#4561
GCTATGCTTT CTTATTGTGC ATACTATGAA
.....
GCTATGCTTT CTTATTGTGC ATACTATGAA

>BS322 1199 to 2683 #1393
#4591
ATGTTTTTCT TCAAAAAGTG TTTATAAGTG
.....
ATGTTTTTCT TCAAAAAGTG TTTATAAGTG

>BS322 1199 to 2683 #1423
#4621
GTAAGTTTAA GAATGGGGTT GACAGCATT
.....
GTAAGTTTAA GAATGGGGTT GACAGCATT

>BS322 1199 to 2683 #1453
#4651
TCTTTTGTGG TTATTTGATT AAACATTTAC
.....
TCTTTTGTGG TTATTTGATT AAACATTTAC

>BS322 1199 to 2683 #1483
#4681
TAATTGTGCA TA
.....
TAATTGTGCA TA

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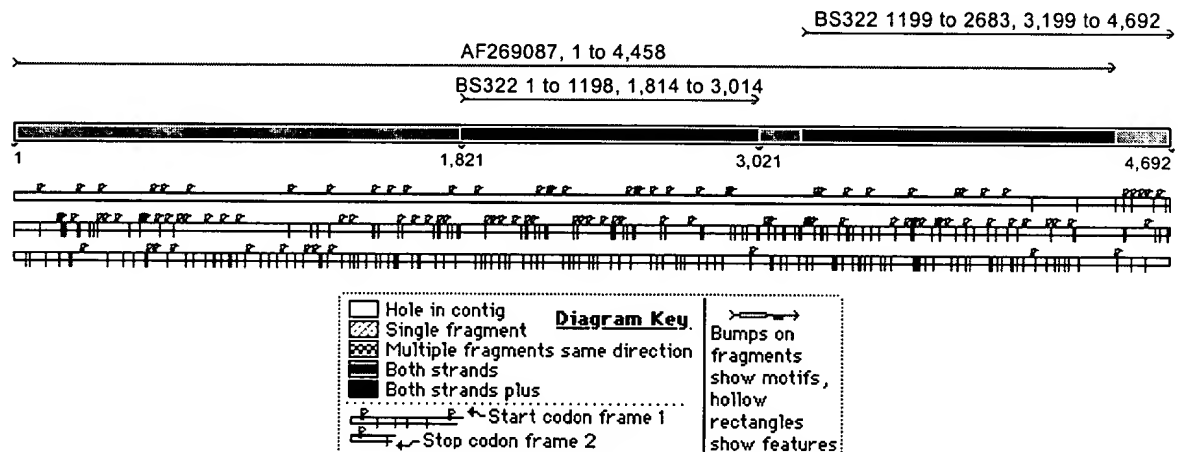
1. BS 322 contains 2683 nucleotides. This sequence was obtained by sequencing Incyte clone 4304443 in house.

2. NY-BR-1 (AF269087) contains 4466 nucleotides.

3. The contig (**below**) shows that BS322 is missing a single stretch of 185 nucleotides that are present in NY-BR-1. These nucleotides are missing between position 1198 and 1199 of BS322. The missing piece is nucleotides 3015 thru 3198 of NY-BR-1(AF269087). The first 45 bases of BS322 are a poor match to AF269087). The remaining bases are almost 100% identical. See BS322 contig summary file.

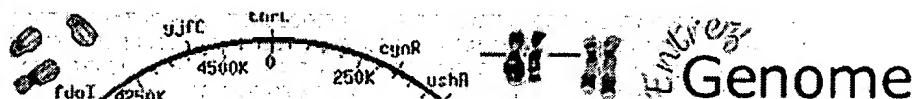
4. It appears that Incyte clone 4304443 is a splice variant of NY-BR-1. The gap occurs in the open reading frame region.

5. The primers used for the NY-BR-1 study were: Forward 2181 to 2202 and Reverse 3088 to 3111(AF269087). These primers are contained within BS322.





results of BLAST



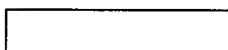
BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig

545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)



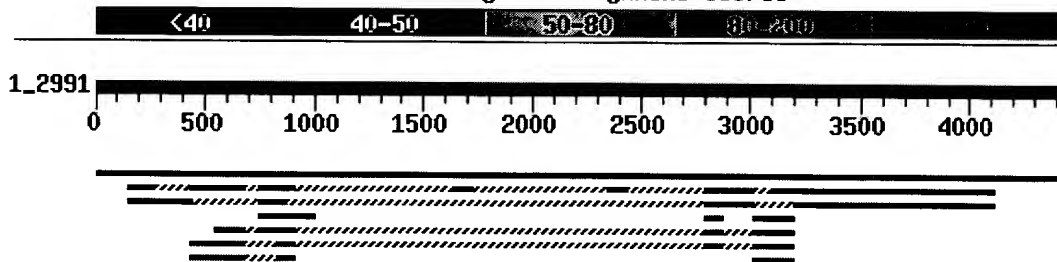
Show positions of the BLAST hits in the human genome using the Entrez
Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast
cancer antigen NY-BR-1 mRNA, complete cds.
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores



Sequences producing significant alignments:

		Score	E
		(bits)	Value
ref NT_008705.14 Hs10_8862	Homo sapiens chromosome 10 genom...	1769	0.0
ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genom...	1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genom...	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genom...	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genom...	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genom...	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genom...	127	5e-26

Alignments

>ref|NT_008705.14|Hs10_8862 Homo sapiens chromosome 10 genomic contig
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Score = 1769 bits (920), Expect = 0.0
Identities = 920/920 (100%)
Strand = Plus / Plus

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Sbjct: 19483239 aggtttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttgaaaa 19483298

Query: 3257 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaaagg 3316
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Sbjct: 19483299 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaaagg 19483358

Query: 3317 aaaataaatactttgaggacattaagatttttaaagaaaagaatgctgaacttcagatga 3376
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Sbjct: 19483359 aaaataaatactttgaggacattaagatttttaaagaaaagaatgctgaacttcagatga 19483418

Query: 3377 ccctaaaactgaaagaggaatcattaactaaaagggcacatctcaatatagtgggcagctta 3436
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Sbjct: 19483419 ccctaaaactgaaagaggaatcattaactaaaagggcacatctcaatatagtgggcagctta 19483478

Query: 3437 aagttctgatagctgagaacacaatgctcacttctaattgaaggaaaaacaagacaaag 3496
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Sbjct: 19483479 aagttctgatagctgagaacacaatgctcacttctaattgaaggaaaaacaagacaaag 19483538

Query: 3497 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 3556
|||||
Sbjct: 19483539 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 19483598

Query: 3557 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 3616
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Sbjct: 19483599 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 19483658

Query: 3617 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataacaatgaggtgc 3676
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Query: 4037 aaaatgaggagatatttaattacaataaccattttaaaaaaccgtatatatcaatatgaaa 4096
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Sbjct: 19484079 aaaatgaggagatatttaattacaataaccattttaaaaaaccgtatatatcaatatgaaa 19484138

Query: 4097 aagagaaagcagaaacagaa 4116
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Score = 1108 bits (576), Expect = 0.0
Identities = 576/576 (100%)
Strand = Plus / Plus

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Query: 809 acacagctgaaagcttgggtggaaaaaacacctgatgaggctgcacccttgggtggaagaa 868
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Sbjct: 19406035 acacagctgaaagcttgggtggaaaaaacacctgatgaggctgcacccttgggtggaagaa 19406094

Query: 869 cacctgacacggctgaaagcttgggtggaaaaaacacctgatgaggctgcaccccttgggtgg 928
|||||
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Query: 929 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagtgcgaacagt 988
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Sbjct: 19406155 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagtgcgaacagt 19406214

Query: 989 cagcagaagaaacacctagggaattacgagtcctgcaaaagaaacatctgagaaattta 1048
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Sbjct: 19406215 cagcagaagaaacacctagggaattacgagtcctgcaaaagaaacatctgagaaattta 19406274

Query: 1049 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 1108
|||||
Sbjct: 19406275 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 19406334

Query: 1109 gggaaattatgagtcctcgcaaaagaaacatctgagaaatttacgtgggcagcaaaaggaa 1168
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Sbjct: 19406335 gggaaattatgagtcctcgcaaaagaaacatctgagaaatttacgtgggcagcaaaaggaa 19406394

Query: 1169 gacctaggaagatcgcatgggagaaaaaagaacacctgtaagactggatgcgtggcaa 1228
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Sbjct: 19406395 gacctaggaagatcgcatgggagaaaaaagaacacctgtaagactggatgcgtggcaa 19406454

Query: 1229 gagtaacatctaataaaaactaaagtgttggaaaaaggaagatctaagatgattgcattg 1288
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Sbjct: 19406455 gagtaacatctaataaaaactaaagtgttggaaaaaggaagatctaagatgattgcattg 19406514

Query: 1289 ctacaaaagaatcatctacaaaagcaagtgccaatg 1324
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Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgccaatg 19406550

Score = 423 bits (220), Expect = e-115
Identities = 220/220 (100%)
Strand = Plus / Plus

Query: 4117 aactcatgagagacaagcagtaagaaacttcttttggagaaacaacagaccagatcttta 4176
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Sbjct: 19495722 aactcatgagagacaagcagtaagaaacttcttttggagaaacaacagaccagatcttta 19495781

Query: 4177 ctcacaactcatgctaggaggccagtcctagcatcaccttatggtgaaaatcttaccaat 4236
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Sbjct: 19495782 ctcacaactcatgctaggaggccagtcctagcatcaccttatggtgaaaatcttaccaat 19495841

Query: 4237 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttctgaagcct 4296
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Query: 4297 acagacataaaaataacagtgtgaagaattacttggttcacg 4336
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Score = 415 bits (216), Expect = e-113
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Strand = Plus / Plus

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Query: 2855 gggaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 2914
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Query: 2915 agttttgtgtactgaaaaagaaactgtcagaagcaaaagaaataaaatcacagttagaga 2974
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Strand = Plus / Plus

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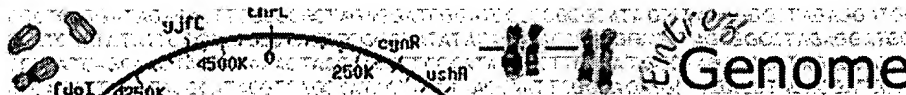
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results of BLAST



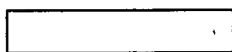
BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig

545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)



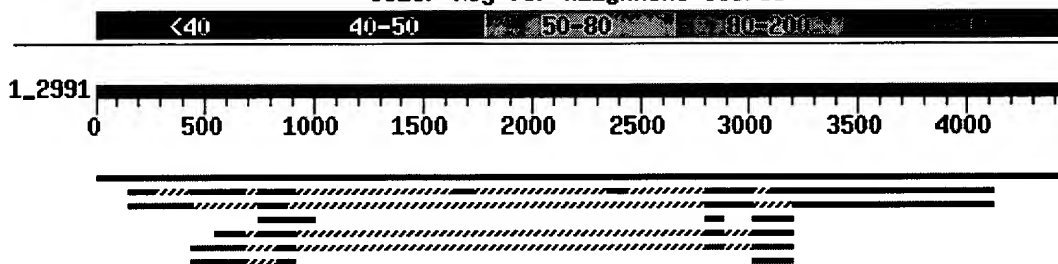
Show positions of the BLAST hits in the human genome using the Entrez
Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast
cancer antigen NY-BR-1 mRNA, complete cds.
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores



Sequences producing significant alignments:				Score (bits)	E Value
ref NT_008705.14 Hs10_8862	Homo sapiens chromosome 10 genom...			1769	0.0
ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genom...			1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genom...			1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genom...			262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...			235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genom...			202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...			192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...			192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genom...			167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genom...			127	5e-26

Alignments

>ref|NT_008705.14|Hs10_8862 Homo sapiens chromosome 10 genomic contig
Length = 20794168

Score = 1769 bits (920), Expect = 0.0
Identities = 920/920 (100%)
Strand = Plus / Plus

```
Query: 3197      aggtttctcacactcatgaaatgaaaattatctcttacatgaaaattgcatgttgaaaa 3256
                |||
Sbjct: 19483239 aggtttctcacactcatgaaatgaaaattatctcttacatgaaaattgcatgttgaaaa 19483298

Query: 3257      aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaagg 3316
                |||
Sbjct: 19483299 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaagg 19483358

Query: 3317      aaaataaatactttgaggacattaagattttaaaagaaaagaatgctgaacttcagatga 3376
                |||
Sbjct: 19483359 aaaataaatactttgaggacattaagattttaaaagaaaagaatgctgaacttcagatga 19483418

Query: 3377      ccctaaaactgaaagaggaatcattaactaaaagggcatctcaatatagtgggcagctta 3436
                |||
Sbjct: 19483419 ccctaaaactgaaagaggaatcattaactaaaagggcatctcaatatagtgggcagctta 19483478

Query: 3437      aagttctgatagctgagaacacaatgctcacttctaaattgaaggaaaaacaagacaaaag 3496
                |||
Sbjct: 19483479 aagttctgatagctgagaacacaatgctcacttctaaattgaaggaaaaacaagacaaaag 19483538

Query: 3497      aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 3556
                |||
Sbjct: 19483539 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 19483598

Query: 3557      atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 3616
                |||
Sbjct: 19483599 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 19483658

Query: 3617      cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataatacaatgaggtgc 3676
                |||
Sbjct: 19483659 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataatacaatgaggtgc 19483718

Query: 3677      tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaaattaatctcaatt 3736
                |||
Sbjct: 19483719 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaaattaatctcaatt 19483778

Query: 3737      atgcaggagatgctctaagagaaaatacattgggttcagaacatgcacaaagagaccaac 3796
                |||
Sbjct: 19483779 atgcaggagatgctctaagagaaaatacattgggttcagaacatgcacaaagagaccaac 19483838

Query: 3797      gtgaaacacagtgtcaaataaggaagctgaacacatgtatcaaacgaacaagataatg 3856
                |||
Sbjct: 19483839 gtgaaacacagtgtcaaataaggaagctgaacacatgtatcaaacgaacaagataatg 19483898

Query: 3857      tgaacaaacacactgaacagcaggagtctctagatcagaaattatttcaactacaaagca 3916
                |||
Sbjct: 19483899 tgaacaaacacactgaacagcaggagtctctagatcagaaattatttcaactacaaagca 19483958

Query: 3917      aaaatatgtggcttcaacagcaattagttcatgcacataagaaagctgacaacaaaagca 3976
                |||
Sbjct: 19483959 aaaatatgtggcttcaacagcaattagttcatgcacataagaaagctgacaacaaaagca 19484018
```

Query: 3977 agataacaattgatattcattttcttgagaggaaaatgcaacatcatctcctaaaagaga 4036
|||||
Sbjct: 19484019 agataacaattgatattcattttcttgagaggaaaatgcaacatcatctcctaaaagaga 19484078

Query: 4037 aaaatgaggagatatttaattacaataaccatttaaaaaaccgtatatatcaatatgaaa 4096
|||||
Sbjct: 19484079 aaaatgaggagatatttaattacaataaccatttaaaaaaccgtatatatcaatatgaaa 19484138

Query: 4097 aagagaaagcagaaacagaa 4116
|||||
Sbjct: 19484139 aagagaaagcagaaacagaa 19484158

Score = 1108 bits (576), Expect = 0.0
Identities = 576/576 (100%)
Strand = Plus / Plus

Query: 749 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcggaaagaacacctg 808
|||||
Sbjct: 19405975 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcggaaagaacacctg 19406034

Query: 809 acacagctgaaagcttgggtgaaaaaacacctgatgaggctgcacccttgggtgaaagaa 868
|||||
Sbjct: 19406035 acacagctgaaagcttgggtgaaaaaacacctgatgaggctgcacccttgggtgaaagaa 19406094

Query: 869 cacctgacacggctgaaagcttgggtgaaaaaacacctgatgaggctgcatccttgggtgg 928
|||||
Sbjct: 19406095 cacctgacacggctgaaagcttgggtgaaaaaacacctgatgaggctgcatccttgggtgg 19406154

Query: 929 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagttcgaacagt 988
|||||
Sbjct: 19406155 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagttcgaacagt 19406214

Query: 989 cagcagaagaacacctagggaaattacgagtcctgcaaaagaacatctgagaaattta 1048
|||||
Sbjct: 19406215 cagcagaagaacacctagggaaattacgagtcctgcaaaagaacatctgagaaattta 19406274

Query: 1049 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 1108
|||||
Sbjct: 19406275 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 19406334

Query: 1109 gggaaattatgagtcctcgcaaaagaacatctgagaaatttacgtgggcagcaaaaggaa 1168
|||||
Sbjct: 19406335 gggaaattatgagtcctcgcaaaagaacatctgagaaatttacgtgggcagcaaaaggaa 19406394

Query: 1169 gacctaggaagatcgcatgggagaaaaaagaaacacctgtaagactggatgcgtggcaa 1228
|||||
Sbjct: 19406395 gacctaggaagatcgcatgggagaaaaaagaaacacctgtaagactggatgcgtggcaa 19406454

Query: 1229 gagtaacatctaataaaactaaagtgtttggaaaaaggaagatctaagatgattgcatgtc 1288
|||||
Sbjct: 19406455 gagtaacatctaataaaactaaagtgtttggaaaaaggaagatctaagatgattgcatgtc 19406514

Query: 1289 ctacaaaagaatcatctacaaaagcaagtgccaatg 1324
|||||

Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgcgaatg 19406550

Score = 423 bits (220), Expect = e-115
Identities = 220/220 (100%)
Strand = Plus / Plus

Query: 4117 aactcatgagagacaagcagtaagaaacttcttttggagaacaacagaccagatcttta 4176
|||||
Sbjct: 19495722 aactcatgagagacaagcagtaagaaacttcttttggagaacaacagaccagatcttta 19495781

Query: 4177 ctcacaactcatgctaggaggccagtcctagcatcaccttatgttgaaaatcttaccat 4236
|||||
Sbjct: 19495782 ctcacaactcatgctaggaggccagtcctagcatcaccttatgttgaaaatcttaccat 19495841

Query: 4237 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttcctgaagcct 4296
|||||
Sbjct: 19495842 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttcctgaagcct 19495901

Query: 4297 acagacataaaaataacagtgtgaagaattacttggtcacg 4336
|||||
Sbjct: 19495902 acagacataaaaataacagtgtgaagaattacttggtcacg 19495941

Score = 415 bits (216), Expect = e-113
Identities = 219/220 (99%), Gaps = 1/220 (0%)
Strand = Plus / Plus

Query: 2796 aga-agattcaactagcctatcaaaaatcttggatacagttcattcttgtgaaagagcaa 2854
|||||
Sbjct: 19480436 agacagattcaactagcctatcaaaaatcttggatacagttcattcttgtgaaagagcaa 19480495

Query: 2855 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 2914
|||||
Sbjct: 19480496 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 19480555

Query: 2915 agttttgtgtactgaaaaagaaactgtcagaagcaaaagaaataaaatcacagttagaga 2974
|||||
Sbjct: 19480556 agttttgtgtactgaaaaagaaactgtcagaagcaaaagaaataaaatcacagttagaga 19480615

Query: 2975 accaaaaagttaaattgggaacaagagctctgcagtgtag 3014
|||||
Sbjct: 19480616 accaaaaagttaaattgggaacaagagctctgcagtgtag 19480655

Score = 362 bits (188), Expect = 1e-96
Identities = 188/188 (100%)
Strand = Plus / Plus

Query: 3013 agattgactttaaaccaagaagaagagaagagaagaaatgccgatattataatgaaaaa 3072
|||||
Sbjct: 19481954 agattgactttaaaccaagaagaagagaagagaagaaatgccgatattataatgaaaaa 19482013

Query: 3073 attagggagaattaggaagaatcgaagagcagcataggaaagagttagaagtgaacaa 3132
|||||

Sbjct: 19482014 attaggaagaattaggaagaatcgaagagcagcataggaaagagttagaagtgaacaa 19482073

Query: 3133 caacttgaacaggctctcagaatacaagatatagaattgaagagtgtagaaagtaatttg 3192

|||||

Sbjct: 19482074 caacttgaacaggctctcagaatacaagatatagaattgaagagtgtagaaagtaatttg 19482133

Query: 3193 aatcaggt 3200

|||||

Sbjct: 19482134 aatcaggt 19482141